

```

10      30      50
-88  GTTGTCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29

70      90      110
-28  CCCTGCTTCTTCCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGGCGTTCGCTCCACGCTCT
-8      M A W L G A S L H V W

130     150     170
32     GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGCGCCAGAGCCCGAGCTGGATTCTGATGGCA 91
12     G W L M L G S C L L A R A Q L D S D G T 31

190     210     230
92     CCATCACTATAGAGGAGCAGATTGTCTCTGTGCTGAAAGCGAAAGTACAATGTGAAGTCA 151
32     I T I E E Q I V L V L K A K V Q C E L N 51

250     270     290
152    ACATCACAGCTCAACTCCAGGAGGGAGGAAGTAATTGTTTCCCTGAATGGGATGGACTCA 211
52     I T A Q L Q E G E G N C F P E W D G L I 71

310     330     350
212    TTTGTTGGCCCAGAGGAACAGTGGGGAAAATATCGGCTGTTCCATGCCCTCCTTATATT 271
72     C W P R G T V G K I S A V P C P Y I Y 91

370     390     410
272    ATGACTTCAACCATAAAGGAGTTGCTTCCGACACTGTAAACCCCAATGGAACATGGGATT 331
92     D F N H K G V A F R H C N P N G T W D F 111

MATCH WITH FIG. 1B

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FIG.1A

MATCH WITH FIG. 1A

332	TTATGCACAGCTTAAATAAACATGGGCCAAATTATTCAGACTGCCTTCGCTTTCTGCAGC	430	450	470	391
112	M H S L N K T W A N Y S D C L R F L Q P				131
392	CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCCTCTATGTAATGTATACCGTTG	490	510	530	451
132	D I S I G K Q E F C E R L Y V M Y T V G				151
452	GCTACTCCATCTCTTTGGTCCCTTGGCTGTGGCTATTCATCATTTGGTTACTTCAGAC	550	570	590	511
152	Y S I S F G S L A V A I L I I G Y F R R				171
512	GATTGCATTGCACACTAGGAACATATATCCACATGCACCTTATTTGTGCTTTTCATGCTGAGAG	610	630	650	571
172	L H C T R N Y I H M H L F V S F M L R A				191
572	CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG	670	690	710	631
192	T S I F V K D R V V H A H I G V K E L E				211
632	AGTCCCTAATAATGCAGGATGACCCACAAAATTCCATTGAGGCAACTTCTGTGGACAAAT	730	750	770	691
212	S L I M Q D D P Q N S I E A T S V D K S				231
		790	810	830	

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1C

1112	1210	1230	1250	1171
372	TCITGGAGTGCATTACATCGTGTTCGTGCGCTGCCTCACTCCTTCACTGGGCTCGGT			391
	F G V H Y I V F V C L P H S F T G L G W			
1172	1270	1290	1310	1231
392	GGGAGATCCGCATGCACCTGTGAGCTCTTCTTCAACTCCTTTCAGGGTTTCTTTGTGCTA			411
	E I R M H C E L F F N S F Q G F F V S I			
1232	1330	1350	1370	1291
412	TCACTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT			431
	I Y C Y C N G E V Q A E V K K M W S R W			
1292	1390	1410	1430	1351
432	GGAATCTCTCCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGCAGATGCGGCTCAG			451
	N L S V D W K R T P P C G S R R C G S V			
1352	1450	1470	1490	1411
452	TGCTCACCACCGTGACGCACAGCACCAGCAGCCAGTCACAGGTGGCGGCAGCACACGCAT			471
	L T T V T H S T S S Q S Q V A A A H A W			
1412	1510	1530	1550	1471
472	GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC			491
	C L S L A K L P R S P A D S L T A T S L			

MATCH WITH FIG. 1E

FIG.1D

MATCH WITH FIG. 1D

1472	TTTTACCTGGCTATGCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA	1570	1590	1610	1531
492	Y L A M S G V T Q S R T A S H T L S T R				511
1532	GGAGCAACAAGGAAGATAGTGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCCA	1630	1650	1670	1591
512	S N K E D S G R Q R D D I L M E K P S R				531
1592	GGCCTATGGAATCTAACCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT	1690	1710	1730	1651
532	P M E S N P D T E G				541
1652	GAATGGACATGTGTGGCTGACTTTTCATGGGCTGGTCCAATGGCTGTTGTGTGAGAGGGC	1750	1770	1790	1711
1712	TTGGCTGATACTCCTATGCCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTACTTAA	1810	1830	1850	1771
1772	TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG	1870	1890	1910	1831
1832	TGTCAATGGAGTAGTTTTATTACCTTCTATTGGCATCAAGTTTTCCTCTAAATTAATGTAT	1930	1950	1970	1891
1892	GGTATTGCTCTGTGATTGTTCA	1990			1914

FIG.1E

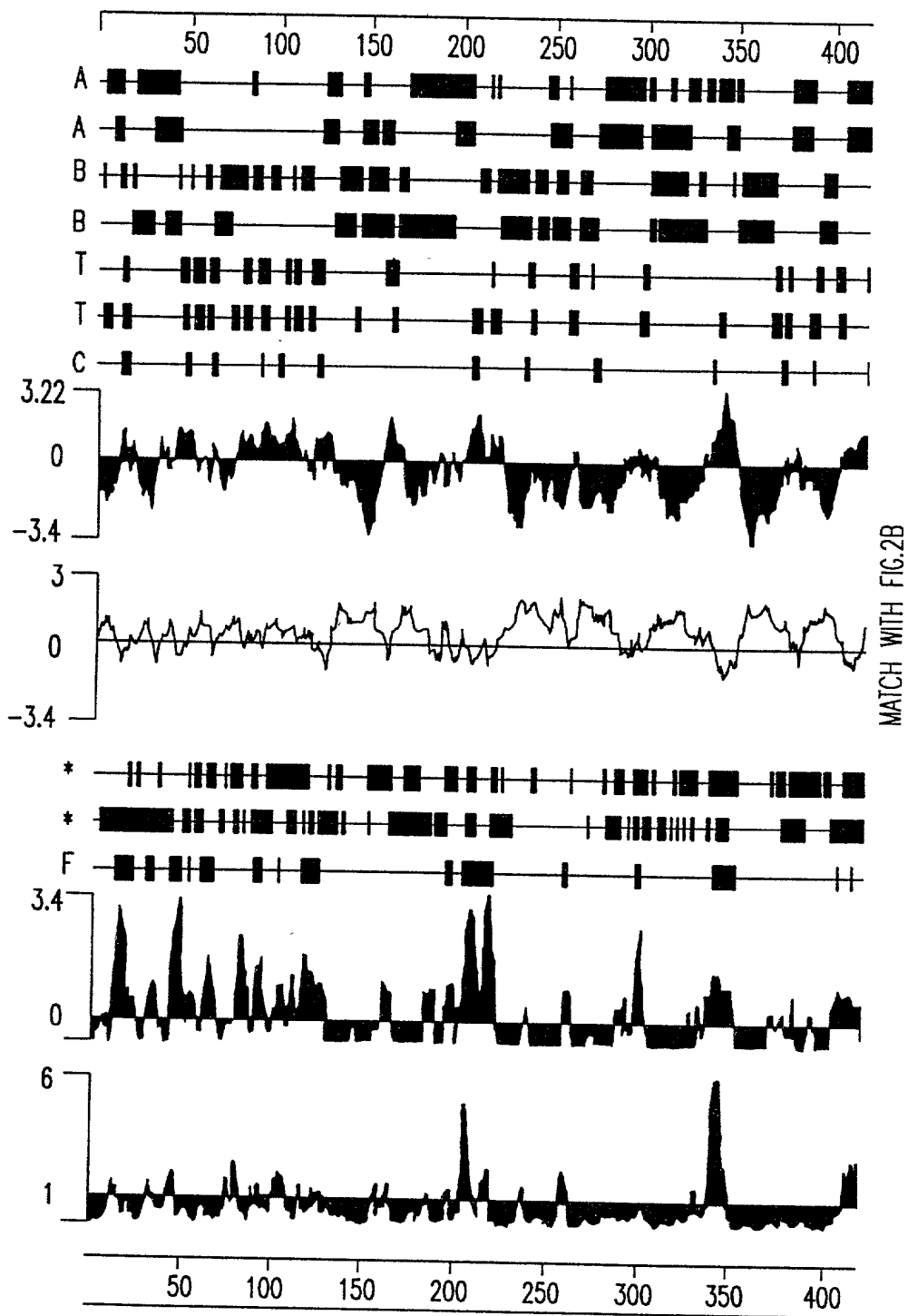


FIG. 2A

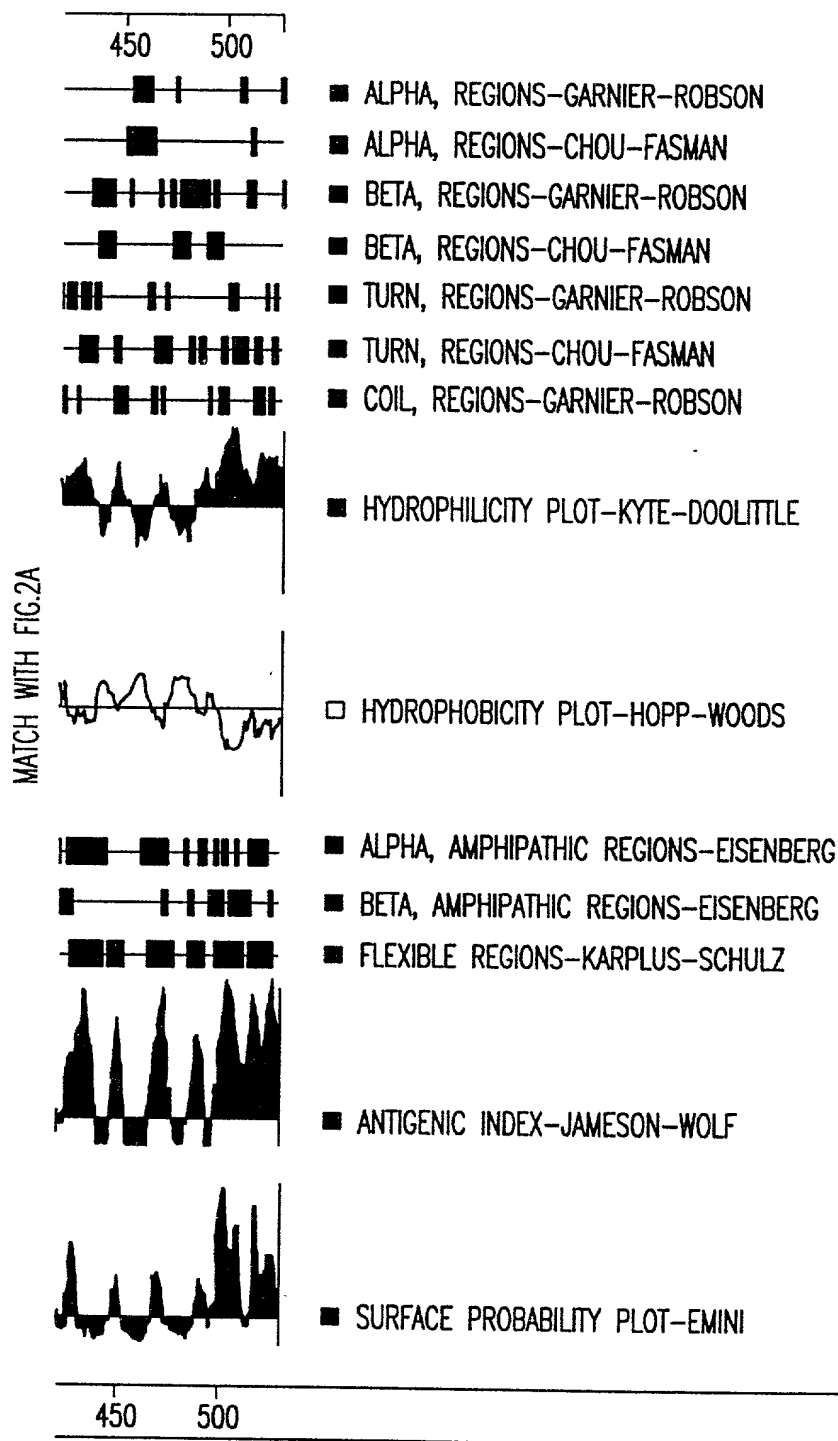


FIG. 2B

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Probability P(N)	N
gp M74445 OPOPTH1R_1	parathyroid hormone receptor [Di...	+3	597	8.2e-204	6
pir S A39286	parathyroid hormone / parathyroid...	+3	597	2.9e-203	6
gp L04308 HUMPTH1R_1	parathyroid hormone receptor [Ho...	+3	580	6.7e-190	5
pir S S29610	parathyroid hormone receptor - h...	+3	580	6.1e-189	5
gp M77184 RATPATH1R_1	parathyroid hormone receptor [Ra...	+3	576	7.7e-188	5
gp X78936 MPH1RPR_1	parathyroid hormone/parathyroid ...	+3	576	7.7e-188	5
pir S A42698	parathyroid hormone and parathyr...	+3	576	7.7e-188	5
gp L34611 MUSPTH1R06_1	parathyroid hormone/parathyroid ...	+3	576	4.1e-174	5
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ...	+3	319	1.2e-98	5
gp M86835 RATVASREC_1	vasoactive intestinal polypeptid...	+3	254	3.1e-91	5

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTH1R_1 parathyroid hormone receptor [Didelphis virginiana]
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

FIG.3A

Match with FIG. 3 A

Query: 729 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYWILVEGLYHNLIFVAFFSDT 908
 I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLH+LIF+AFFS+
 Sbjct: 253 ITEEELRAFTPEPPADKAGFVGCRAVTVFLYFLTNYWILVEGLYHLSLIFMAFFSEK 312

Query: 909 KYLWGFILIGWFPAAFAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILF 1088
 KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF
 Sbjct: 313 KYLWGFILFGLPAFVAVVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILF 372

Query: 1089 LNTVRVLATKIWEITNAVGHDTRKQYRKLAKSTLVLVFVGVHYIVFVCLPHS 1244
 +N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
 Sbjct: 373 INIIRVLATKLRETNAGRCSTRQYRKLKSTLVLMPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTW 446
 +G C PEWD ++CWP G GK+ AVPCP YIYDFNHHKG A+R C+ NG+W+ + N+TW
 Sbjct: 102 DGFCLPEWDNIVCWPAGVPGKVAVVPCPDYIYDFNHHKGRAYRRCDNGSWELVPGNNRTW 161

Query: 447 ANYSDCLRFL 476
 ANYS+C++FL
 Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KOEFCERLVMTYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLVFSFMLRATSIFV 677
 ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHMHLVFSFMLRA SIF+
 Match with FIG. 3 C

FIG.3B

MATCH WITH FIG. 3B

236

Sbjct: 177 EREVFDRLGMIYTVGYISLSGLTAVLILGYFRRLLHCTRNYYTHMHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESIMQD 740
 KD V+++ + E+E + ++

Sbjct: 237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNSFQGFVSIICYCNGEVQAEVKMWSRWNLSDWKRTPPCGS 1424
 +G+ W+++MH E+ FNSFQGFV+IYC+CNGEVQAE+KK WSRW L++D+KR GS 485

Sbjct: 427 SGILWQVMHYEMLFNSFQGFVAIIYCFNGEVQAEIKKSWSRWTLALDFKRRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLDSDGTITIEEQIVLVKAKVQCELNITAQLQEGE 269
 A +D+D IT EEQI+L+ A+ QCE + L+ E

Sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576
 +S + A A + H LPGYV

Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIG. 3C